RAW SEQUENCE LISTING   DATE: 01/26/2002
PATENT APPLICATION: US/09/890,229A   TIME: 13:02:00

Input Set : A:\574900_1.txt
Output Set: N:\CRF3\01262002\I890229A.raw

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 3 <110> APPLICANT: Bramley, Peter Michael
 4          Harker, Mark
 6 <120> TITLE OF INVENTION: Manipulating Isoprenoid Expression
 8 <130> FILE REFERENCE: B0192/7031
10 <140> CURRENT APPLICATION NUMBER: 09/890,229A
11 <141> CURRENT FILING DATE: 2000-01-28
13 <150> PRIOR APPLICATION NUMBER: GB 9901902.8
14 <151> PRIOR FILING DATE: 1999-01-28
16 <160> NUMBER OF SEQ ID NOS: 12
18 <170> SOFTWARE: PatentIn version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 640
22 <212> TYPE: PRT
23 <213> ORGANISM: Synechocystis sp.
25 <400> SEQUENCE: 1
27 Met His Ile Ser Glu Leu Thr His Pro Asn Glu Leu Lys Gly Leu Ser
28 1               5                   10                  15
30 Ile Arg Glu Leu Glu Glu Val Ser Arg Gln Ile Arg Glu Lys His Leu
31             20                  25                  30
33 Gln Thr Val Ala Thr Ser Gly Gly His Leu Gly Pro Gly Leu Gly Val
34         35                  40                  45
36 Val Glu Leu Thr Val Ala Leu Tyr Ser Thr Leu Asp Leu Asp Lys Asp
37     50                  55                  60
39 Arg Val Ile Trp Asp Val Gly His Gln Ala Tyr Pro His Lys Met Leu
40 65                  70                  75                  80
42 Thr Gly Arg Tyr His Asp Phe His Thr Leu Arg Gln Lys Asp Gly Val
43                 85                  90                  95
45 Ala Gly Tyr Leu Lys Arg Ser Glu Ser Arg Phe Asp His Phe Gly Ala
46             100                 105                 110
48 Gly His Ala Ser Thr Ser Ile Ser Ala Gly Leu Gly Met Ala Leu Ala
49             115                 120                 125
51 Arg Asp Ala Lys Gly Glu Asp Phe Lys Val Val Ser Ile Ile Gly Asp
52         130                 135                 140
54 Gly Ala Leu Thr Gly Gly Met Ala Leu Glu Ala Ile Asn His Ala Gly
55 145                 150                 155                 160
57 His Leu Pro His Thr Arg Leu Met Val Ile Leu Asn Asp Asn Glu Met
58                 165                 170                 175
60 Ser Ile Ser Pro Asn Val Gly Ala Ile Ser Arg Tyr Leu Asn Lys Val
61             180                 185                 190
63 Arg Leu Ser Ser Pro Met Gln Phe Leu Thr Asp Asn Leu Glu Glu Gln
64         195                 200                 205
66 Ile Lys His Leu Pro Phe Val Gly Asp Ser Leu Thr Pro Glu Met Glu
67     210                 215                 220
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Input Set : A:\574900_1.txt
Output Set: N:\CRF3\01262002\I890229A.raw

```
69  Arg Val Lys Glu Gly Met Lys Arg Leu Val Val Pro Lys Val Gly Ala
70  225             230             235                 240
72  Val Ile Glu Glu Leu Gly Phe Lys Tyr Phe Gly Pro Ile Asp Gly His
73              245             250             255
75  Ser Leu Gln Glu Leu Ile Asp Thr Phe Lys Gln Ala Glu Lys Val Pro
76          260             265             270
78  Gly Pro Val Phe Val His Val Ser Thr Thr Lys Gly Lys Gly Tyr Asp
79          275             280             285
81  Leu Ala Glu Lys Asp Gln Val Gly Tyr His Ala Gln Ser Pro Phe Asn
82      290             295             300
84  Leu Ser Thr Gly Lys Ala Tyr Pro Ser Ser Lys Pro Lys Pro Pro Ser
85  305             310             315                 320
87  Tyr Ser Lys Val Phe Ala His Thr Leu Thr Thr Leu Ala Lys Glu Asn
88              325             330             335
90  Pro Asn Ile Val Gly Ile Thr Ala Ala Met Ala Thr Gly Thr Gly Leu
91              340             345             350
93  Asp Lys Leu Gln Ala Lys Leu Pro Lys Gln Tyr Val Asp Val Gly Ile
94          355             360             365
96  Ala Glu Gln His Ala Val Thr Leu Ala Ala Gly Met Ala Cys Glu Gly
97      370             375             380
99  Ile Arg Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Gly Tyr
100 385             390             395                 400
102 Asp Gln Ile Ile His Asp Val Cys Ile Gln Lys Leu Pro Val Phe Phe
103             405             410             415
105 Cys Leu Asp Arg Ala Gly Ile Val Gly Ala Asp Gly Pro Thr His Gln
106             420             425             430
108 Gly Met Tyr Asp Ile Ala Tyr Leu Arg Cys Ile Pro Asn Leu Val Leu
109             435             440             445
111 Met Ala Pro Lys Asp Glu Ala Glu Leu Gln Gln Met Leu Val Thr Gly
112     450             455             460
114 Val Asn Tyr Thr Gly Gly Ala Ile Ala Met Arg Tyr Pro Arg Gly Asn
115 465             470             475                 480
117 Gly Ile Gly Val Pro Leu Met Glu Glu Gly Trp Glu Pro Leu Glu Ile
118             485             490             495
120 Gly Lys Ala Glu Ile Leu Arg Ser Gly Asp Asp Val Leu Leu Leu Gly
121             500             505             510
123 Tyr Gly Ser Met Val Tyr Pro Ala Leu Gln Thr Ala Glu Leu Leu His
124             515             520             525
126 Glu His Gly Ile Glu Ala Thr Val Val Asn Ala Arg Phe Val Lys Pro
127     530             535             540
129 Leu Asp Thr Glu Leu Ile Leu Pro Leu Ala Glu Arg Ile Gly Lys Val
130 545             550             555                 560
132 Val Thr Met Glu Glu Gly Cys Leu Met Gly Gly Phe Gly Ser Ala Val
133             565             570             575
135 Ala Glu Ala Leu Met Asp Asn Asn Val Leu Val Pro Leu Lys Arg Leu
136             580             585             590
138 Gly Val Pro Asp Ile Leu Val Asp His Ala Thr Pro Glu Gln Ser Thr
139             595             600             605
141 Val Asp Leu Gly Leu Thr Pro Ala Gln Met Ala Gln Asn Ile Met Ala
```

Input Set : A:\574900_1.txt
Output Set: N:\CRF3\01262002\I890229A.raw

```
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144 Ser Leu Phe Lys Thr Glu Thr Glu Ser Val Val Ala Pro Gly Val Ser
145 625                  630                  635                  640
147 <210> SEQ ID NO: 2
148 <211> LENGTH: 633
149 <212> TYPE: PRT
150 <213> ORGANISM: Bacillus subtilis
152 <400> SEQUENCE: 2
154 Met Asp Leu Leu Ser Ile Gln Asp Pro Ser Phe Leu Lys Asn Met Ser
155 1            5                  10                  15
157 Ile Asp Glu Leu Glu Lys Leu Ser Asp Glu Ile Arg Gln Phe Leu Ile
158          20                  25                  30
160 Thr Ser Leu Ser Ala Ser Gly Gly His Ile Gly Pro Asn Leu Gly Val
161          35                  40                  45
163 Val Glu Leu Thr Val Ala Leu His Lys Glu Phe Asn Ser Pro Lys Asp
164          50                  55                  60
166 Lys Phe Leu Trp Asp Val Gly His Gln Ser Tyr Val His Lys Leu Leu
167 65                  70                  75                  80
169 Thr Gly Arg Gly Lys Glu Phe Ala Thr Leu Arg Gln Tyr Lys Gly Leu
170          85                  90                  95
172 Cys Gly Phe Pro Lys Arg Ser Glu Ser Glu His Asp Val Trp Glu Thr
173          100                 105                 110
175 Gly His Ser Ser Thr Ser Leu Ser Gly Ala Met Gly Met Ala Ala Ala
176          115                 120                 125
178 Arg Asp Ile Lys Gly Thr Asp Glu Tyr Ile Ile Pro Ile Ile Gly Asp
179          130                 135                 140
181 Gly Ala Leu Thr Gly Gly Met Ala Leu Glu Ala Leu Asn His Ile Gly
182 145                 150                 155                 160
184 Asp Glu Lys Lys Asp Met Ile Val Ile Leu Asn Asp Asn Glu Met Ser
185          165                 170                 175
187 Ile Ala Pro Asn Val Gly Ala Ile His Ser Met Leu Gly Arg Leu Arg
188          180                 185                 190
190 Thr Ala Gly Lys Tyr Gln Trp Val Lys Asp Glu Leu Glu Tyr Leu Phe
191          195                 200                 205
193 Lys Lys Ile Pro Ala Val Gly Gly Lys Leu Ala Ala Thr Ala Glu Arg
194          210                 215                 220
196 Val Lys Asp Ser Leu Lys Tyr Met Leu Val Ser Gly Met Phe Phe Glu
197 225                 230                 235                 240
199 Glu Leu Gly Phe Thr Tyr Leu Gly Pro Val Asp Gly His Ser Tyr His
200          245                 250                 255
202 Glu Leu Ile Glu Asn Leu Gln Tyr Ala Lys Lys Thr Lys Gly Pro Val
203          260                 265                 270
205 Leu Leu His Val Ile Thr Lys Lys Gly Lys Gly Tyr Lys Pro Ala Glu
206          275                 280                 285
208 Thr Asp Thr Ile Gly Thr Trp His Gly Thr Gly Pro Tyr Lys Ile Asn
209          290                 295                 300
211 Thr Gly Asp Phe Val Lys Pro Lys Ala Ala Ala Pro Ser Trp Ser Gly
212 305                 310                 315                 320
214 Leu Val Ser Gly Thr Val Gln Arg Met Ala Arg Glu Asp Gly Arg Ile
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RAW SEQUENCE LISTING   DATE: 01/26/2002
PATENT APPLICATION: US/09/890,229A   TIME: 13:02:00

Input Set : A:\574900_1.txt
Output Set: N:\CRF3\01262002\I890229A.raw

```
215                 325              330              335
217 Val Ala Ile Thr Pro Ala Met Pro Val Gly Ser Lys Leu Glu Gly Phe
218             340              345              350
220 Ala Lys Glu Phe Pro Asp Arg Met Phe Asp Val Gly Ile Ala Glu Gln
221         355              360              365
223 His Ala Ala Thr Met Ala Ala Ala Met Ala Met Gln Gly Met Lys Pro
224         370              375              380
226 Phe Leu Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp Gln Val
227 385              390              395              400
229 Val His Asp Ile Cys Arg Gln Asn Ala Asn Val Phe Ile Gly Ile Asp
230             405              410              415
232 Arg Ala Gly Leu Val Gly Ala Asp Gly Glu Thr His Gln Gly Val Phe
233         420              425              430
235 Asp Ile Ala Phe Met Arg His Ile Pro Asn Met Val Leu Met Met Pro
236         435              440              445
238 Lys Asp Glu Asn Glu Gly Gln His Met Val His Thr Ala Leu Ser Tyr
239     450              455              460
241 Asp Glu Gly Pro Ile Ala Met Arg Phe Pro Arg Gly Asn Gly Leu Gly
242 465              470              475              480
244 Val Lys Met Asp Glu Gln Leu Lys Thr Ile Pro Ile Gly Thr Trp Glu
245             485              490              495
247 Val Leu Arg Pro Gly Asn Asp Ala Val Ile Leu Thr Phe Gly Thr Thr
248         500              505              510
250 Ile Glu Met Ala Ile Glu Ala Ala Glu Glu Leu Gln Lys Glu Gly Leu
251         515              520              525
253 Ser Val Arg Val Val Asn Ala Arg Phe Ile Lys Pro Ile Asp Glu Lys
254     530              535              540
256 Met Met Lys Ser Ile Leu Lys Glu Gly Leu Pro Ile Leu Thr Ile Glu
257 545              550              555              560
259 Glu Ala Val Leu Glu Gly Gly Phe Gly Ser Ile Leu Glu Phe Ala
260             565              570              575
262 His Asp Gln Gly Glu Tyr His Thr Pro Ile Asp Arg Met Gly Ile Pro
263         580              585              590
265 Asp Arg Phe Ile Glu His Gly Ser Val Thr Ala Leu Leu Glu Glu Ile
266         595              600              605
268 Gly Leu Thr Lys Gln Gln Val Ala Asn Arg Ile Arg Leu Leu Met Pro
269     610              615              620
271 Pro Lys Thr His Lys Gly Ile Gly Ser
272 625                 630
274 <210> SEQ ID NO: 3
275 <211> LENGTH: 620
276 <212> TYPE: PRT
277 <213> ORGANISM: Escherichia coli
279 <400> SEQUENCE: 3
281 Met Ser Phe Asp Ile Ala Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser
282 1               5               10              15
284 Thr Gln Glu Leu Arg Leu Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys
285         20              25              30
287 Asp Glu Leu Arg Arg Tyr Leu Leu Asp Ser Val Ser Arg Ser Ser Gly
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RAW SEQUENCE LISTING   DATE: 01/26/2002
PATENT APPLICATION: US/09/890,229A   TIME: 13:02:00

Input Set: A:\574900_1.txt
Output Set: N:\CRF3\01262002\I890229A.raw

```
288        35               40               45
290 His Phe Ala Ser Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His
291     50               55               60
293 Tyr Val Tyr Asn Thr Pro Phe Asp Gln Leu Ile Trp Asp Val Gly His
294 65               70               75               80
296 Gln Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly
297             85               90               95
299 Thr Ile Arg Gln Lys Gly Gly Leu His Pro Phe Pro Trp Arg Gly Glu
300             100              105              110
302 Ser Glu Tyr Asp Val Leu Ser Val Gly His Ser Ser Thr Ser Ile Ser
303         115              120              125
305 Ala Gly Ile Gly Ile Ala Val Ala Ala Glu Lys Glu Gly Lys Asn Arg
306     130              135              140
308 Arg Thr Val Cys Val Ile Gly Asp Gly Ala Ile Thr Ala Gly Met Ala
309 145              150              155              160
311 Phe Glu Ala Met Asn His Ala Gly Asp Ile Arg Pro Asp Met Leu Val
312             165              170              175
314 Ile Leu Asn Asp Asn Glu Met Ser Ile Ser Glu Asn Val Gly Ala Leu
315             180              185              190
317 Asn Asn His Leu Ala Gln Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu
318         195              200              205
320 Arg Glu Gly Gly Lys Lys Val Phe Ser Gly Val Pro Pro Ile Lys Glu
321     210              215              220
323 Leu Leu Lys Arg Thr Glu Glu His Ile Lys Gly Met Val Val Pro Gly
324 225              230              235              240
326 Thr Leu Phe Glu Glu Leu Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly
327             245              250              255
329 His Asp Val Leu Gly Leu Ile Thr Thr Leu Lys Asn Met Arg Asp Leu
330         260              265              270
332 Lys Gly Pro Gln Phe Leu His Ile Met Thr Lys Lys Gly Arg Gly Tyr
333     275              280              285
335 Glu Pro Ala Glu Lys Asp Pro Ile Thr Phe His Ala Val Pro Lys Phe
336     290              295              300
338 Asp Pro Ser Ser Gly Cys Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser
339 305              310              315              320
341 Tyr Ser Lys Ile Phe Gly Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp
342             325              330              335
344 Asn Lys Leu Met Ala Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Met
345             340              345              350
347 Val Glu Phe Ser Arg Lys Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile
348         355              360              365
350 Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly
351     370              375              380
353 Tyr Lys Pro Ile Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr
354 385              390              395              400
356 Asp Gln Val Leu His Asp Val Ala Ile Gln Lys Leu Pro Val Leu Phe
357             405              410              415
359 Ala Ile Asp Arg Ala Gly Ile Val Gly Ala Asp Gly Gln Thr His Gln
360         420              425              430
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The use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 01/26/2002
PATENT APPLICATION: US/09/890,229A   TIME: 13:02:01

Input Set : A:\574900_1.txt
Output Set: N:\CRF3\01262002\I890229A.raw

L:525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1064 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1066 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6